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SEQ ID No. 1.

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CCATCAAGGA GATCTCCGGC ACCGTCAAGC TGCCGGGGTC CAAGTCGCTT TCCAACCGGA   180
TCCTCCTACT CGCCGCCCTG TCCGAGGGGA CAACAGTGGT TGATAACCTG CTGAACAGTG   240
AGGATGTCCA CTACATGCTC GGGGCCTTGA GGACTCTTGG TCTCTCTGTC GAAGCGGACA   300
AAGCTCCCAA AAGACCTGTA GTTGTTGGCT GTGGTGGAAA GTTCCCAGTT GAGGATGCTA   360
AAGAGGAAGT GCAGCTCTTC TTGGGGAATG CTGGAACTGC AATGCGGCCA TTGACAGCAG   420
CTGTTACTGC TGCTGGTGGA AATGCAACTT ACGTGCTTGA TGGAGTACCA AGAATGAGGG   480
AGAGACCCAT TGGCGACTTG GTTGTCGGAT TGAAGCAGCT TGGTGCAGAT GTTGATTGTT   540
TCCTTGGCAC TGACTGCCCA CCTGTTCGTG TCAATGGAAT CGGAGGGCTA CCTGGTGGCA   600
AGGTCAAGCT GTCTGGCTCC ATCAGCAGTC AGTACTTGAG TGCCTTGCTG ATGGCTGCTC   660
CTTTGGCTCT TGGGGATGTG GAGATTGAAA TCATTGATAA ATTAATCTCC ATTCCGTACG   720
TCGAAATGAC ATTGAGATTG ATGGAGCGTT TTGGTGTGAA AGCAGAGCAT TCTGATAGCT   780
GGGACAGATT CTACATTAAG GGAGGTCAAA AATACAAGTC CCCTAAAAAT GCCTATGTTG   840
AAGGTGATGC CTCAAGCGCA AGCTATTTCT TGGCTGGTGC TGCAATTACT GGAGGGACTG   900
TGACTGTGGA AGGTTGTGGC ACCACCAGTT TGCAGGGTGA TGTGAAGTTT GCTGAGGTAC   960
TGGAGATGAT GGGAGCGAAG GTTACATGGA CCGAGACTAG CGTAACTGTT ACTGGCCCAC  1020
CGCGGGAGCC ATTTGGGAGG AAACACCTCA AGGCGATTGA TGTCAACATG AACAAGATGC  1080
CTGATGTCGC CATGACTCTT GCTGTGGTTG CCCTCTTTGC CGATGGCCCG ACAGCCATCA  1140
GAGACGTGGC TTCCTGGAGA GTAAAGGAGA CCGAGAGGAT GGTTGCGATC CGGACGGAGC  1200
TAACCAAGCT GGGAGCATCT GTTGAGGAAG GGCCGGACTA CTGCATCATC ACGCCGCCGG  1260
AGAAGCTGAA CGTGACGGCG ATCGACACGT ACGACGACCA CAGGATGGCC ATGGCCTTCT  1320
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CCTTCCCCGA CTACTTCGAT GTGCTGAGCA CTTTCGTCAA GAATTAATAA AGCGTGCGAT  1440
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TTTCTATTTC GGATCTTAAG TTTGTGCACT GTAAGCCAAA TTTCATTTCA AGAGTGGTTC  1620
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SEQ ID N . 2.

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TCC GGC ACC GTC AAG CTG CCG GGG TCC AAG TCG CTT TCC AAC CGG ATC        95
Ser Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile
 15                  20                  25                  30

CTC CTA CTC GCC GCC CTG TCC GAG GGG ACA ACA GTG GTT GAT AAC CTG       143
Leu Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu
                 35                  40                  45

CTG AAC AGT GAG GAT GTC CAC TAC ATG CTC GGG GCC TTG AGG ACT CTT       191
Leu Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu
             50                  55                  60

GGT CTC TCT GTC GAA GCG GAC AAA GCT GCC AAA AGA GCT GTA GTT GTT       239
Gly Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val
         65                  70                  75

GGC TGT GGT GGA AAG TTC CCA GTT GAG GAT GCT AAA GAG GAA GTG CAG       287
Gly Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln
     80                  85                  90

CTC TTC TTG GGG AAT GCT GGA ACT GCA ATG CGG CCA TTG ACA GCA GCT       335
Leu Phe Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala
 95                 100                 105                 110

GTT ACT GCT GCT GGT GGA AAT GCA ACT TAC GTG CTT GAT GGA GTA CCA       383
Val Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro
                115                 120                 125

AGA ATG AGG GAG AGA CCC ATT GGC GAC TTG GTT GTC GGA TTG AAG CAG       431
Arg Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln
            130                 135                 140

CTT GGT GCA GAT GTT GAT TGT TTC CTT GGC ACT GAC TGC CCA CCT GTT       479
Leu Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val
        145                 150                 155

CGT GTC AAT GGA ATC GGA GGG CTA CCT GGT GGC AAG GTC AAG CTG TCT       527
Arg Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser
    160                 165                 170

GGC TCC ATC AGC AGT CAG TAC TTG AGT GCC TTG CTG ATG GCT GCT CCT       575
Gly Ser Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro
175                 180                 185                 190

TTG GCT CTT GGG GAT GTG GAG ATT GAA ATC ATT GAT AAA TTA ATC TCC       623
Leu Ala Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser
                195                 200                 205

ATT CCG TAC GTC GAA ATG ACA TTG AGA TTG ATG GAG CGT TTT GGT GTG       671
Ile Pro Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val
            210                 215                 220

AAA GCA GAG CAT TCT GAT AGC TGG GAC AGA TTC TAC ATT AAG GGA GGT       719
Lys Ala Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly
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SEQ ID No. 2 (continuati n).

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Ser Ala Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val
255 260 265 270

ACT GTG GAA GGT TGT GGC ACC ACC AGT TTG CAG GGT GAT GTG AAG TTT 863
Thr Val Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe
275 280 285

GCT GAG GTA CTG GAG ATG ATG GGA GCG AAG GTT ACA TGG ACC GAG ACT 911
Ala Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr
290 295 300

AGC GTA ACT GTT ACT GGC CCA CCG CGG GAG CCA TTT GGG AGG AAA CAC 959
Ser Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His
305 310 315

CTC AAG GCG ATT GAT GTC AAC ATG AAC AAG ATG CCT GAT GTC GCC ATG 1007
Leu Lys Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met
320 325 330

ACT CTT GCT GTG GTT GCC CTC TTT GCC GAT GGC CCG ACA GCC ATC AGA 1055
Thr Leu Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg
335 340 345 350

GAC GTG GCT TCC TGG AGA GTA AAG GAG ACC GAG AGG ATG GTT GCG ATC 1103
Asp Val Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile
355 360 365

CGG ACG GAG CTA ACC AAG CTG GGA GCA TCT GTT GAG GAA GGG CCG GAC 1151
Arg Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp
370 375 380

TAC TGC ATC ATC ACG CCG CCG GAG AAG CTG AAC GTG ACG GCG ATC GAC 1199
Tyr Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp
385 390 395

ACG TAC GAC GAC CAC AGG ATG GCC ATG GCC TTC TCC CTT GCC GCC TGT 1247
Thr Tyr Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys
400 405 410

GCC GAG GTC CCC GTC ACC ATC CGG GAC CCT GGG TGC ACC CGG AAG ACC 1295
Ala Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr
415 420 425 430

TTC CCC GAC TAC TTC GAT GTG CTG AGC ACT TTC GTC AAG AAT 1337
Phe Pro Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
435 440

TAA 1340

SEQ ID No. 3.

Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly
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Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu
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Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn
35 40 45

Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
50 55 60

Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
65 70 75 80

Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110

Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
130 135 140

Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
145 150 155 160

Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Ala
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
195 200 205

Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
210 215 220

Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
245 250 255

Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
260 265 270

Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
290 295 300

Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
305 310 315 320

Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
355 360 365

Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
405 410 415

Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430

Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
435 440

SEQ ID No. 4.

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CCATG GCC GGC GCC GAG GAG ATC GTG CTG CAG CCC ATC AAG GAG ATC      47
      Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile
      1           5                   10

TCC GGC ACC GTC AAG CTG CCG GGG TCC AAG TCG CTT TCC AAC CGG ATC    95
Ser Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile
15                  20                  25                  30

CTC CTA CTC GCC GCC CTG TCC GAG GGG ACA ACA GTG GTT GAT AAC CTG   143
Leu Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu
                35                  40                  45

CTG AAC AGT GAG GAT GTC CAC TAC ATG CTC GGG GCC TTG AGG ACT CTT   191
Leu Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu
            50                  55                  60

GGT CTC TCT GTC GAA GCG GAC AAA GCT GCC AAA AGA GCT GTA GTT GTT   239
Gly Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val
        65                  70                  75

GGC TGT GGT GGA AAG TTC CCA GTT GAG GAT GCT AAA GAG GAA GTG CAG   287
Gly Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln
    80                  85                  90

CTC TTC TTG GGG AAT GCT GGA ATC GCA ATG CGG TCC TTG ACA GCA GCT   335
Leu Phe Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala
95                  100                 105                 110

GTT ACT GCT GCT GGT GGA AAT GCA ACT TAC GTG CTT GAT GGA GTA CCA   383
Val Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro
                115                 120                 125

AGA ATG AGG GAG AGA CCC ATT GGC GAC TTG GTT GTC GGA TTG AAG CAG   431
Arg Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln
            130                 135                 140

CTT GGT GCA GAT GTT GAT TGT TTC CTT GGC ACT GAC TGC CCA CCT GTT   479
Leu Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val
        145                 150                 155

CGT GTC AAT GGA ATC GGA GGG CTA CCT GGT GGC AAG GTC AAG CTG TCT   527
Arg Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser
    160                 165                 170

GGC TCC ATC AGC AGT CAG TAC TTG AGT GCC TTG CTG ATG GCT GCT CCT   575
Gly Ser Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro
175                 180                 185                 190

TTG GCT CTT GGG GAT GTG GAG ATT GAA ATC ATT GAT AAA TTA ATC TCC   623
Leu Ala Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser
                195                 200                 205

ATT CCG TAC GTC GAA ATG ACA TTG AGA TTG ATG GAG CGT TTT GGT GTG   671
Ile Pro Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val
            210                 215                 220

AAA GCA GAG CAT TCT GAT AGC TGG GAC AGA TTC TAC ATT AAG GGA GGT   719
Lys Ala Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly
        225                 230                 235
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SEQ ID N . 4 (c ntinuation).

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    240                 245                 250

AGC GCA AGC TAT TTC TTG GCT GGT GCT GCA ATT ACT GGA GGG ACT GTG      815
Ser Ala Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val
255                 260                 265                 270

ACT GTG GAA GGT TGT GGC ACC ACC AGT TTG CAG GGT GAT GTG AAG TTT      863
Thr Val Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe
                275                 280                 285

GCT GAG GTA CTG GAG ATG ATG GGA GCG AAG GTT ACA TGG ACC GAG ACT      911
Ala Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr
            290                 295                 300

AGC GTA ACT GTT ACT GGC CCA CCG GAG CCA TTT GGG AGG AAA CAC      959
Ser Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His
        305                 310                 315

CTC AAG GCG ATT GAT GTC AAC ATG AAC AAG ATG CCT GAT GTC GCC ATG     1007
Leu Lys Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met
    320                 325                 330

ACT CTT GCT GTG GTT GCC CTC TTT GCC GAT GGC CCG ACA GCC ATC AGA     1055
Thr Leu Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg
335                 340                 345                 350

GAC GTG GCT TCC TGG AGA GTA AAG GAG ACC GAG AGG ATG GTT GCG ATC     1103
Asp Val Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile
                355                 360                 365

CGG ACG GAG CTA ACC AAG CTG GGA GCA TCT GTT GAG GAA GGG CCG GAC     1151
Arg Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp
            370                 375                 380

TAC TGC ATC ATC ACG CCG CCG GAG AAG CTG AAC GTG ACG GCG ATC GAC     1199
Tyr Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp
        385                 390                 395

ACG TAC GAC GAC CAC AGG ATG GCG ATG GCC TTC TCC CTT GCC GCC TGT     1247
Thr Tyr Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys
    400                 405                 410

GCC GAG GTC CCC GTC ACC ATC CGG GAC CCT GGG TGC ACC CGG AAG ACC     1295
Ala Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr
415                 420                 425                 430

TTC CCC GAC TAC TTC GAT GTG CTG AGC ACT TTC GTC AAG AAT      1337
Phe Pro Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
                435                 440

TAA                                                         1340
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SEQ ID No. 5.

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35 40 45

Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
50 55 60

Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
65 70 75 80

Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
85 90 95

Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala Val Thr
100 105 110

Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
130 135 140

Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
145 150 155 160

Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
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Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
195 200 205

Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
210 215 220

Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
245 250 255

Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
260 265 270

Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
290 295 300

Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
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Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
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Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
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Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
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SEQ ID No. 6.

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SEQ ID No. 7.

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TCTTGCTTCG AAGTTCTGTA TAACCAGATT TGTCTGTGTG CGATTGTCAT TACCTAGCCG 300

TGTATCGAGA ACTAGGGTTT TCGAGTCAAT TTTGCCCCTT TTGGTTATAT CTGGTTCGAT 360

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SEQUENCE LISTING

<110> DEROSE, Richard
CHAUBET, Nicole
GIGOT, Claude (deceased)

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Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
20 25 30

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Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly
         50                  55                  60

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     65                  70                  75

tgt ggt gga aag ttc cca gtt gag gat gct aaa gag gaa gtg cag ctc   290
Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu
 80                  85                  90                  95

ttc ttg ggg aat gct gga act gca atg cgg cca ttg aca gca gct gtt   338
Phe Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val
                100                 105                 110

act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga   386
Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg
            115                 120                 125

atg agg gag aga ccc att ggc gac ttg gtt gtc gga ttg aag cag ctt   434
Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu
        130                 135                 140

ggt gca gat gtt gat tgt ttc ctt ggc act gac tgc cca cct gtt cgt   482
Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg
    145                 150                 155

gtc aat gga atc gga ggg cta cct ggt ggc aag gtc aag ctg tct ggc   530
Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly
160                 165                 170                 175

tcc atc agc agt cag tac ttg agt gcc ttg ctg atg gct gct cct ttg   578
Ser Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu
                180                 185                 190

gct ctt ggg gat gtg gag att gaa atc att gat aaa tta atc tcc att   626
Ala Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile
            195                 200                 205

ccg tac gtc gaa atg aca ttg aga ttg atg gag cgt ttt ggt gtg aaa   674
Pro Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys
        210                 215                 220

gca gag cat tct gat agc tgg gac aga ttc tac att aag gga ggt caa   722
Ala Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln
    225                 230                 235

aaa tac aag tcc cct aaa aat gcc tat gtt gaa ggt gat gcc tca agc   770
Lys Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser
240                 245                 250                 255

gca agc tat ttc ttg gct ggt gct gca att act gga ggg act gtg act   818
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```
Ala Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr
                260                 265                 270

gtg gaa ggt tgt ggc acc acc agt ttg cag ggt gat gtg aag ttt gct   866
Val Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala
            275                 280                 285

gag gta ctg gag atg atg gga gcg aag gtt aca tgg acc gag act agc   914
Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser
        290                 295                 300

gta act gtt act ggc cca ccg cgg gag cca ttt ggg agg aaa cac ctc   962
Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu
    305                 310                 315

aag gcg att gat gtc aac atg aac aag atg cct gat gtc gcc atg act  1010
Lys Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr
320                 325                 330                 335

ctt gct gtg gtt gcc ctc ttt gcc gat ggc ccg aca gcc atc aga gac  1058
Leu Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp
                340                 345                 350

gtg gct tcc tgg aga gta aag gag acc gag agg atg gtt gcg atc cgg  1106
Val Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg
            355                 360                 365

acg gag cta acc aag ctg gga gca tct gtt gag gaa ggg ccg gac tac  1154
Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr
        370                 375                 380

tgc atc atc acg ccg ccg gag aag ctg aac gtg acg gcg atc gac acg  1202
Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr
    385                 390                 395

tac gac gac cac agg atg gcc atg gcc ttc tcc ctt gcc gcc tgt gcc  1250
Tyr Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala
400                 405                 410                 415

gag gtc ccc gtc acc atc cgg gac cct ggg tgc acc cgg aag acc ttc  1298
Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe
                420                 425                 430

ccc gac tac ttc gat gtg ctg agc act ttc gtc aag aat taa          1340
Pro Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
            435                 440
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<210> 3
<211> 444
<212> PRT
<213> Zea mays

<400> 3

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Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly
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1               5                  10                  15
Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu
            20                  25                  30
Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn
        35                  40                  45
Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
    50                  55                  60
Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
65                  70                  75                  80
Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
                85                  90                  95
Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
            100                 105                 110
Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
        115                 120                 125
Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
    130                 135                 140
Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
145                 150                 155                 160
Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
                165                 170                 175
Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Ala
            180                 185                 190
Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
        195                 200                 205
Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
    210                 215                 220
Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
225                 230                 235                 240
Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
                245                 250                 255
Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
            260                 265                 270
Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
        275                 280                 285
Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
    290                 295                 300
```

```
Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
305                 310                 315                 320

Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
                325                 330                 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
            340                 345                 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
        355                 360                 365

Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
    370                 375                 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
385                 390                 395                 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
                405                 410                 415

Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
            420                 425                 430

Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
        435                 440
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<210> 4
<211> 1340
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (6)..(1337)

<400> 4

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      Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser
        1               5                  10                  15

ggc acc gtc aag ctg ccg ggg tcc aag tcg ctt tcc aac cgg atc ctc   98
Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
                20                  25                  30

cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg   146
Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu
            35                  40                  45

aac agt gag gat gtc cac tac atg ctc ggg gcc ttg agg act ctt ggt   194
Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly
        50                  55                  60

ctc tct gtc gaa gcg gac aaa gct gcc aaa aga gct gta gtt gtt ggc   242
```

```
Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly
     65                  70                  75

tgt ggt gga aag ttc cca gtt gag gat gct aaa gag gaa gtg cag ctc   290
Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu
 80                  85                  90                  95

ttc ttg ggg aat gct gga atc gca atg cgg tcc ttg aca gca gct gtt   338
Phe Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala Val
                100                 105                 110

act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga   386
Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg
            115                 120                 125

atg agg gag aga ccc att ggc gac ttg gtt gtc gga ttg aag cag ctt   434
Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu
        130                 135                 140

ggt gca gat gtt gat tgt ttc ctt ggc act gac tgc cca cct gtt cgt   482
Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg
    145                 150                 155

gtc aat gga atc gga ggg cta cct ggt ggc aag gtc aag ctg tct ggc   530
Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly
160                 165                 170                 175

tcc atc agc agt cag tac ttg agt gcc ttg ctg atg gct gct cct ttg   578
Ser Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu
                180                 185                 190

gct ctt ggg gat gtg gag att gaa atc att gat aaa tta atc tcc att   626
Ala Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile
            195                 200                 205

ccg tac gtc gaa atg aca ttg aga ttg atg gag cgt ttt ggt gtg aaa   674
Pro Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys
        210                 215                 220

gca gag cat tct gat agc tgg gac aga ttc tac att aag gga ggt caa   722
Ala Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln
    225                 230                 235

aaa tac aag tcc cct aaa aat gcc tat gtt gaa ggt gat gcc tca agc   770
Lys Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser
240                 245                 250                 255

gca agc tat ttc ttg gct ggt gct gca att act gga ggg act gtg act   818
Ala Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr
                260                 265                 270

gtg gaa ggt tgt ggc acc acc agt ttg cag ggt gat gtg aag ttt gct   866
Val Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala
            275                 280                 285
```

```
gag gta ctg gag atg atg gga gcg aag gtt aca tgg acc gag act agc   914
Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser
        290                 295                 300

gta act gtt act ggc cca ccg cgg gag cca ttt ggg agg aaa cac ctc   962
Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu
    305                 310                 315

aag gcg att gat gtc aac atg aac aag atg cct gat gtc gcc atg act   1010
Lys Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr
320                 325                 330                 335

ctt gct gtg gtt gcc ctc ttt gcc gat ggc ccg aca gcc atc aga gac   1058
Leu Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp
                340                 345                 350

gtg gct tcc tgg aga gta aag gag acc gag agg atg gtt gcg atc cgg   1106
Val Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg
            355                 360                 365

acg gag cta acc aag ctg gga gca tct gtt gag gaa ggg ccg gac tac   1154
Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr
        370                 375                 380

tgc atc atc acg ccg ccg gag aag ctg aac gtg acg gcg atc gac acg   1202
Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr
    385                 390                 395

tac gac gac cac agg atg gcg atg gcc ttc tcc ctt gcc gcc tgt gcc   1250
Tyr Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala
400                 405                 410                 415

gag gtc ccc gtc acc atc cgg gac cct ggg tgc acc cgg aag acc ttc   1298
Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe
                420                 425                 430

ccc gac tac ttc gat gtg ctg agc act ttc gtc aag aat taa           1340
Pro Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
            435                 440
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<210> 5
<211> 444
<212> PRT
<213> Zea mays

<400> 5

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Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly
  1               5                  10                  15

Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu
            20                  25                  30

Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn
        35                  40                  45
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Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
50 55 60

Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
65 70 75 80

Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
85 90 95

Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala Val Thr
100 105 110

Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
130 135 140

Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
145 150 155 160

Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Ala
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
195 200 205

Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
210 215 220

Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
245 250 255

Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
260 265 270

Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
290 295 300

Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
305 310 315 320

Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val

340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
355 360 365

Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
405 410 415

Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430

Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
435 440

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<212> DNA
<213> Zea mays

<400> 6
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aactactgga atcgctcgat aggtggtacg aaattaggcg agattagttt ctattcttgg 120

ccattatctt gtttcttcgc cgaatgatct tccgtataaa gattttaggt tagagatgaa 180

tcgtatagct agatttcatc accagatagt ttctttgtct agaatctctg aaattctcga 240

tagttttcac atgtgtaaat agattgttct tattcggcga ttgttgatta gggttttgat 300

tttcttgatt atgcgattgc aattagggat tttctttggt tttgtgttga tcttacgata 360

cattcctgca attgaatacg tatggatcta aatcttgtta atttgttgaa cagatccc 418

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<213> Zea mays

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cgggttttgt cccattccag tttgaaaata aacgtccgtc ttttaagttt gctggatcga 180

taaacctgtg aagattgagt ctagtcgatt tattggatga tccattcttc atcgtttttt 240

tcttgcttcg aagttctgta taaccagatt tgtctgtgtg cgattgtcat tacctagccg 300

tgtatcgaga actagggttt tcgagtcaat tttgcccctt ttggttatat ctggttcgat 360

aacgattcat ctggattagg gttttaagtg gtgacgttta gtattccaat ttcttcaaaa 420

tttagttatg gataatgaaa atcccgaatt gactgttcaa tttcttgtta aatgcgcaga 480

tcccgggatc tgcg 494

<210> 8
<211> 20
<212> DNA
<213> Zea mays

<400> 8
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<210> 9
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<400> 9
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<210> 10
<211> 10
<212> DNA
<213> Zea mays

<400> 10
aattcccggg 10

<210> 11
<211> 38
<212> DNA
<213> Zea mays

<400> 11
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<210> 12
<211> 41
<212> DNA
<213> Zea mays

<400> 12
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<210> 13
<211> 37
<212> DNA
<213> Zea mays

<400> 13
gcacgatctc ctcggcgccg gccatggagc tcggctc 37

<210> 14
<211> 25
<212> DNA
<213> Zea mays

<400> 14
ccacaggatg gcgatggcct tctcc 25

<210> 15
<211> 33
<212> DNA
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<400> 15
gaatgctgga atcgcaatgc ggccattgac agc 33

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<210> 18
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<210> 19

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<400> 19
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<400> 20
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cagatcccgg gatctgcg 18

<210> 22
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<400> 22
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